

SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: Au-Young, Janice

(ii) TITLE OF THE INVENTION: NOVEL HUMAN STEM CELL ANTIGENS

(iii) NUMBER OF SEQUENCES: 26

(iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
- (B) STREET: 3174 Porter Drive
- (C) CITY: Palo Alto
- (D) STATE: CA
- (E) COUNTRY: U.S.
- (F) ZIP: 94304

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Diskette
- (B) COMPUTER: IBM Compatible
- (C) OPERATING SYSTEM: DOS
- (D) SOFTWARE: FastSEQ Version 1.5

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: To Be Assigned
- (B) FILING DATE: Filed Herewith

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Billings, Lucy J.
- (B) REGISTRATION NUMBER: 36,749
- (C) REFERENCE/DOCKET NUMBER: PF-0066 US

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: 415-855-0555
- (B) TELEFAX: 415-845-4166

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: SCAH-1
- (B) CLONE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met Lys Ile Phe Leu Pro Val Leu Leu Ala Ala Leu Leu Gly Val Glu
1 5 10 15
Arg Ala Ser Ser Leu Met Cys Phe Ser Cys Leu Asn Gln Lys Ser Asn
20 25 30

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Leu Tyr Cys Leu Lys Pro Thr Ile Cys Ser Asp Gln Asp Asn Tyr Cys
35 40 45
Val Thr Val Ser Ala Ser Ala Gly Ile Gly Asn Leu Val Thr Phe Gly
50 55 60
His Ser Leu Ser Lys Thr Cys Ser Pro Ala Cys Pro Ile Pro Glu Gly
65 70 75 80
Val Asn Val Gly Val Ala Ser Met Gly Ile Ser Cys Cys Gln Ser Phe
85 90 95
Leu Cys Asn Phe Ser Ala Ala Asp Gly Gly Leu Arg Ala Ser Val Thr
100 105 110
Leu Leu Gly Ala Gly Leu Leu Ser Leu Xaa Pro Ala Leu Leu Arg
115 120 125
Phe Gly PRO
130

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 123 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:
(A) LIBRARY: SCAH-2
(B) CLONE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Lys Ala Val Leu Leu Ala Leu Leu Met Ala Gly Leu Ala Leu Gln
1 5 10 15
Pro Gly Thr Ala Leu Leu Cys Tyr Ser Cys Lys Ala Gln Val Ser Asn
20 25 30
Glu Asp Cys Leu Gln Val Glu Asn Cys Thr Gln Leu Gly Glu Gln Cys
35 40 45
Trp Thr Ala Arg Ile Arg Ala Val Gly Leu Leu Thr Val Ile Ser Lys
50 55 60
Gly Cys Ser Leu Asn Cys Val Asp Asp Ser Gln Asp Tyr Tyr Val Gly
65 70 75 80
Lys Lys Asn Ile Thr Cys Cys Asp Thr Asp Leu Cys Asn Xaa Ser Gly
85 90 95
Ala His Ala Leu Gln Pro Ala Ala Ala Ile Leu Ala Leu Leu Pro Ala
100 105 110
Leu Gly Leu Leu Leu Trp Gly Pro Gly Gln Leu
115 120

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 537 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

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(vii) IMMEDIATE SOURCE:
(A) LIBRARY: SCAH-1
(B) CLONE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

NAGGANGGTG	GGGGACCCAN	GGGTCCAGAG	CGCAGTCGG	GTCGGAGCTY	CGWCCAGGCT	60
GCTGGTACCT	GCGTCCGCC	GGCGAGCAGG	ACAGGCTGCT	TTGGTTGTG	ACCTCCAGGC	120
AGGACGCCA	TCCTCTCCAG	AATGAAGATC	TTCTTGCCAG	TGCTGCTGGC	TGCCCTTCTG	180
GGTGTGGAGC	GAGCCAGCTC	GCTGATGTGC	TTCTCCTGCT	TGAACCAGAA	GAGCAATCTG	240
TACTGCTGA	AGCCGACCAT	CTGCTCCGAC	CAGGACAAC	ACTGGGTGAC	TGTGCTGCT	300
AGTGCCGGCA	TTGGGAATCT	CGTGACATTT	GGCCACAGCC	TGAGCAAGAC	CTGTTCCCCG	360
GCCTGCCCA	TCCCAGAAGG	CGTCAATGTT	GGTGTGGCTT	CCATGGGCAT	CAGCTGCTGC	420
CAGAGCTTTC	TGTGCAATT	CAGTGCGGCC	GATGGCGGGC	TGCGGGCAAG	CGTCACCCCTG	480
CTGGGTGCCG	GGCTGCTGCT	GAGCCTGWTG	CCGGCCCTGC	TGCGGTITGG	CCCCCTGA	537

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 494 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
(A) LIBRARY: SCAH-2
(B) CLONE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GTGACCATGA	AGGCTGTGCT	GCTTGCCTG	TTGATGGCAG	GCTTGGCCCT	GCAGCCAGGC	60
ACTGCCCTGC	TGTGCTACTC	CTGCAAAGCC	CAGGTGAGCA	ACGAGGACTG	CCTGCAGGTG	120
GAGAACTGCA	CCCAGCTGGG	GGAGCAGTGC	TGACCGCGC	GCATCCGC	AGTTGGCCTC	180
CTGACCGTCA	TCAGCAAAGG	CTGCAGCTTG	AACTGCGTGG	ATGACTCACA	GGACTACTAC	240
GTGGGCAAGA	AGAACATCAC	GTGCTGTGAC	ACCGACTTGT	GCAACGSCAG	CGGGGCCCAT	300
GCCCTGCAGC	CGGCTGCCGC	CATCCTGCG	CTGCTCCCTG	CACTCGGCCT	GCTGCTCTGG	360
GGACCCGGCC	AGCTATAGGC	TCTGGGGGGC	CCCGMTGCAG	CCCACACTGG	GTGTGGTGCC	420
CCAAGGCC	TGTGSCACTC	CTMACAGACC	TGGGCCAGT	GGGAGSCTGT	CTCTNGGTTC	480
CTGAGGCACA	TCCT					494

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 136 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:
(A) LIBRARY: GenBank
(B) CLONE: 434660

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

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Met Ser Ala Thr Ser Asn Met Arg Val Phe Leu Pro Val Leu Leu Ala
1 5 10 15
Ala Leu Leu Gly Met Glu Gln Val His Ser Leu Met Cys Phe Ser Cys
20 25 30
Thr Asp Gin Lys Asn Asn Ile Asn Cys Leu Trp Pro Val Ser Cys Gln
35 40 45
Glu Lys Asp His Tyr Cys Ile Thr Leu Ser Ala Ala Ala Gly Phe Gly
50 55 60
Asn Val Asn Leu Gly Tyr Thr Leu Asn Lys Gly Cys Ser Pro Ile Cys
65 70 75 80
Pro Ser Glu Asn Val Asn Leu Asn Leu Gly Val Ala Ser Val Asn Ser
85 90 95
Tyr Cys Cys Gin Ser Ser Phe Cys Asn Phe Ser Ala Ala Gly Leu Gly
100 105 110
Leu Arg Ala Ser Ile Pro Leu Leu Gly Leu Gly Leu Leu Ser Leu
115 120 125
Leu Ala Leu Leu Gln Leu Ser Pro
130 135

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: 1199651

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Ser Thr Thr Ser Ser Met Arg Val Phe Ser Ile Val Leu Gln Ala
1 5 10 15
His Leu Leu Gly Val Glu Leu Val Pro Ser Leu Ile Cys Ser Ser Cys
20 25 30
Thr His Gln Lys Ser Asn Ile Asn Pro Pro Trp Pro Val Ala Cys Lys
35 40 45
Asp Thr Gly Asn Tyr Cys Ile Met Leu Phe Ser Ala Val Gly Phe Gly
50 55 60
Asn Val Asn Leu Gly Tyr Thr Leu Asn Thr Gly Cys Ser Gln Ser Cys
65 70 75 80
Pro His Glu Asn Ile Asn Ile Asn Pro Gly Val Ala Ser Val Asn Ser
85 90 95
Tyr Gln Ser Ser Phe Cys Asn Phe Ser Asn Ala Cys Leu
100 105

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
(A) LIBRARY: THP1PEB01
(B) CLONE: 72518

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CCTGAAGCCG ACCATCTGNT CCGACCAGGN CAACTACTGN GTGACTGTGT CTGCTAGTGC	60
CGGCATTGG AATCTTGTGC CATTNGACA CAGCCTNAGC AAGACCTNTT CCCCAGGCTN	120
NCCCATCCCA GAAGGNGTCA ATNATNGT	148

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 196 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
(A) LIBRARY: THP1PLB02
(B) CLONE: 155838

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CGGACAGGCT GCTTTGGTTT GTNACCTCCA GGCAGGACGG CCATCCTCTC CAGAATGAAG	60
ATCTTCTTGC CANTGCTGCT GGCTGCCCTT CTNGGTGTGG AGCGAGCCAG CTCGCTGATG	120
TGCTTCTCT GCTTNAACCA GAAGAGCAAT CTGTACTGCC TGAAGCCGAC CATCTGCTCC	180
GACCAGGNCA ACTACT	196

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 278 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
(A) LIBRARY: HNT2RAT01
(B) CLONE: 486681

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GTTCGGGGAG CTCGGCCAGG CTGCTGGTAC CTGGCGTCCGC CCGGCGAGCA GGACAGGCTG	60
CTTGGTTTG TGACCTNCAG GCAGGACGGC CATCCTCTNC AGAATGAAGA TCTTCTTGCC	120
AGTGCTGCTG GNTGCCCTTC TGGGTGTGGA GCGAGCCAGC TNGCTGATGT GCTTCTTCTG	180
CTTGAACCAG AAGAGCAATC TGTACTGCTG AAGCCGACCA TCTGTTGAC CAGGNCAACT	240
ACTGCGTGAC TGTGTCTGCT AGTGNCGGCA TTGGGAAT	278

(2) INFORMATION FOR SEQ ID NO:10:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 262 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(viii) IMMEDIATE SOURCE:

- (A) LIBRARY: BRSTTUT01
- (B) CLONE: 604702

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GGTTGGGGGA	GCTCGGCCAG	GCTGCTGGTA	CCTGGTCCG	CCCGGCAGAC	AGGACAGGCT	60
GCTTGGTT	TGACCTCCA	GGCAGGACGG	CCATCCTCTC	CAGAATGAAG	ATCTCTTG	120
CAGTGCTGCT	GGCTGCCCTT	CTGGGTGTGG	AGCGAGCCAG	CTCGCTGATG	TGCTTCTCCT	180
GCTTGAACCA	GAAGAGCAAT	CTGTACTGCC	TGAAGCCGAC	CATCTGCTCC	GACCAGGACA	240
ACTACTGCGT	GACTGTGTCT	GC				262

(2) INFORMATION FOR SEQ ID NO:11:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 289 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(viii) IMMEDIATE SOURCE:

- (A) LIBRARY: BRSTTUT01
- (B) CLONE: 606246

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GTTCGGGGAG	CTCGGCCAGG	CTGCTGGTAC	CTGCGTCCGC	CCGGCGAGCA	GGACAGGCTG	60
CTTTGGTTTG	TGACCTCCAG	GCAGGACGGC	CATCCTCTCC	AGAATGAAGA	TCTTCTTGCC	120
AGTGCTGCTG	GCTGCCCTTC	TGGGTGTGGA	GCGAGCCAGC	TCGCTGATGT	GCTTCTCCTG	180
CTTGAACCAAG	AAGAGCAATC	TGTACTGCC	GAAGCCGACC	ATCTGCTCCG	ACCAGGACAA	240
CTACTGCGTGC	ACTGTGTCTG	CTAGTGCCGG	CATTGGGAAT	CTCGTGACA		289

(2) INFORMATION FOR SEQ ID NO:12:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 335 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(viii) IMMEDIATE SOURCE:

- (A) LIBRARY: BRSTNOT03
- (B) CLONE: 637479

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

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GGTCGGGGAG	CTCGGCCAGG	CTGCTGGTAC	CTGCGTCCGC	CCGGCGAGCA	GGACAGGCTG	60
CTTTGGTTTG	TGACCTCCAG	GCAGGACGGC	CATCCTNTCC	AGAATGAAGA	TCTTCTTGC	120
AGTGCTGCTG	GCTGCCCTTC	TGGGTGTGGA	GCGAGCCAGC	TCGCTGATGT	GCTTCTNCTG	180
CTTGAACCAAG	AAGAGCAATC	TGTACTGCCT	GAAGCCGACG	ATCTGCTCCG	ACCAGGACAA	240
CTACTGCCGTG	ACTGTGTCTG	CTAGTGCCGG	CATTGGGAAT	CTCGTACAT	TTGGNCACAG	300
CTGAGCAAGA	CCTGTTNCCC	GGNCTGCCCG	ATNCG			335

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 261 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BRSTNOT03
- (B) CLONE: 641178

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GGTCGGGGAG	GCTCGGCCAG	GCTGCTGGTA	CCTGCGTCCG	CCCGGCGAGC	AGGACAGGCT	60
GCTTGGTTT	GTGACCTNCA	GGCAGGACGG	CCATCCTCTC	CAGAATGAAG	ATCTTNTTGC	120
CAGTGCTNCT	NGCTGCCCTT	CTGGGTGTGG	AGCGAGCCAG	CTNGCTGATG	TGCTTCTTCT	180
GCTTGAACCA	GAAGAGCAAT	TGTACTGTC	TGAAGCCGAC	CATTGCTNC	GACCAGGNCA	240
ACTACTGTGT	GACTGTNTNT	T				261

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 287 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BRSTNOT03
- (B) CLONE: 642012

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

AAGCCGACCA	TCTGCTCCGA	CCAGGACAAC	TACTGCGTGA	CTGTGTCTGC	TAGTGCCGGC	60
ATTGGGAATC	TCGTGACATT	TGGCCACAGC	CTGAGCAAGA	CCTGTTCCCC	GGCCTGCC	120
ATCCCAGAAG	GCGTCAATGT	TGGTGTGGCT	TCCATGGGNA	TCAGCTGCTG	CCAGAGCTTT	180
CTGTGCAATT	TCAGTGCAGC	CGATGGGGGG	CTGCGGGCAA	GCGTCACCCCT	GCTGGGTGCC	240
GGGCTGCTGC	TGAGCTGCTG	CCGGCCCTGC	TGCGGTTGG	CCCCTGA		287

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 294 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

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(D) TOPOLOGY: linear

(11) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: LUNGTUT02
- (B) CLONE: 690697

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

AGGANGGTGG	GGGACCCANG	GGTCCGGCCA	NGGGTCCGAG	NTTCGGCAAG	GTNCTGGTAN	60
CTGCGTNCGG	CCGGCGAGCA	GGACANGNTG	CTTGGTTTG	TGACTNCAGG	NAGGACGGCC	120
ATNCTTNCAG	AATTAAGATC	TTNTTGCAG	TGCTGNTGGC	TGCCCTTCIG	GGTGTNGAGC	180
GAGCCAGTNG	NTGATGTGNT	TNTTCTGCTT	GAACCAAGAAG	AGCAATCTGT	ACTGCCTGAA	240
GCCGACCATG	TGGTTCGACC	AGGGCAACTA	NTGCGTGA	GTGTCTGTAG	TGNC	294

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: LUNGNOT03
- (B) CLONE: 728784

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

TCCAGAGCGC	GCGAGGTTCG	GGGAGCTCGG	CCAGGCTGCT	GGTACCTGCG	TCCGCCCCGGC	60
GGACAGGCTG	CTTGGTTTG	TGACCTCCAG	GCAGGACGGC	CATCCTCTCC	AGAATGAAGA	120
TCTTCTTGCC	AGTGCTGCTG	GCTGCCCTTC	TGGGTGTGGA	GCGAGCCAGC	TCGCTGATGT	180
GCTTCTCTG	CTTGAACCAAG	AAGAGCAATC	TGTACTGCCT	GAAGCCGACC	ATCTGCTCCG	240
ACCAGGACAA	CTACTGNGTG	ACTGTG				266

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 280 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: OVARNOT03
- (B) CLONE: 797584

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

TNGGNCCNGG	TGNTGGTACC	GNGTCCGCC	GGCGAGCAGA	CAGGCTGCTT	TGGTTTGTGA	60
CCTCCAGGNA	GGACGGCCAT	CCTCTCCAGA	ATGAAGATCT	TCTTGCCAGT	GCTGCTGGCT	120
GGCCCTTCTGG	GTGTGGAGCG	AGCCANCTCG	CTGATGTGCT	TCTCCTGCTT	GAACCAGAAG	180

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AGCAATCTGT ACTGCCTGAA GCCGACCATC TGCTNCGACC AGGNCAACTA CTGCGTGACT 240
GTGTCTGCTA GTGCCGGCAT TGGGAATCTC GTGACAATTG 280

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 275 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: PROSTUT04
- (B) CLONE: 831396

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

AGTTNGGGGA GCTCCGTCAG GCTNCTGGTA CCTGCGTCCG CCCGGCGAGC AGGACAGGNT 60
GCTTTANTTT NTGACCTNCA GGCAGGACGG CCATNCTATN CAGAATGAAG ATCTTATTGC 120
CANTGCTGNT GGNNTGNCCCTT NTGNGTGTNG AGCGAGCCAG NTCNATGATG TGNTTNTCCT 180
GNTTGAACCA GAAGAGCAAT NTGTANTGCC TGAAGCCGAC CATNTGNTCC GACCAGGACA 240
ANTANTGCGT GANTGTGTNT GCTAGTGCCG GCATT 275

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 297 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BRSTNOT05
- (B) CLONE: 897330

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GAACCAGAAG AGCAATNTGT ACTGCCTGAA GCCGACCATN TGCTNCGACC AGGNCAACTA 60
CTGCGTGACT GTGTNTGCTA GTGCCGGCAT TGGGAATNTN GTGACATTTG GCCACAGCCT 120
GAGCAAGACC TGTCCCCNGG NCTGCCCAT CCCAGAAGGC GTCAATGTTG GTGTGGNTTC 180
CATGGGCATC AGCTGCTGCC AGAGCTTTNT GTGCAATTTC AGTGCAGCCG ATGGNGGGCT 240
GNGGGCAAGC GTCACCCNTGN TGGGTGCCGG GNTGNTGNTG AGCCTGGTGN CGGCCCT 297

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

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(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: 509840

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Met Lys Ala Phe Leu Phe Ala Val Leu Ala Ala Val Leu Cys Val Glu
1 5 10 15
Arg Ala His Thr Leu Ile Cys Phe Ser Cys Ser Asp Ala Ser Ser Asn
20 25 30
Trp Ala Cys Leu Thr Pro Val Lys Cys Ala Glu Asn Glu Glu His Cys
35 40 45
Val Thr Thr Tyr Val Gly Val Gly Gly Lys Ser Gly Gln Ser
50 55 60
Ile Ser Lys Gly Cys Ser Pro Val Cys Pro Ser Ala Gly Ile Asn Leu
65 70 75 80
Gly Ile Ala Ala Ala Ser Val Tyr Cys Cys Asp Ser Phe Leu Cys Asn
85 90 95
Ile Ser Gly Ser Ser Ser Val Lys Ala Ser Tyr Ala Val Leu Ala Leu
100 105 110
Gly Ile Leu Val Ser Phe Val Tyr Val Leu Arg Ala Arg Glu
115 120 125

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 286 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: UTRSNOT01
- (B) CLONE: 588615

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

ATGGCAGGCT	TGGCCCTGCA	GCCAGGNACT	GCCCTGCTGT	GCTACTCCTG	CAAAGCCCAG	60
GTGAGCAACG	AGGACTGCCT	GCAGGTGGAG	AACTGCACCC	AGCTGGGGGA	GCAGTGCTGG	120
ACCGCGCGCA	TNCGGCAGTT	GGCCTNCTGA	CCGTCATCAG	CAAAGGCTGC	AGCTTGAACT	180
GCCTGGATGA	CTNACAGGAC	TACTACGTGG	GCAAGAAAGAA	CATCACGTGC	TGTGACANCG	240
ACTTGTGCAA	NGGCANCGGG	GCCCCATGCC	TGCAGNCGGC	TNTCGC		286

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 251 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: UTRSNOT01
- (B) CLONE: 590328

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

AANAGGTAT TAGGNGGGAA NGAGGACNAN NANGTGTGN GACANCGACT TGTGAAACGG	60
CAGCGGGGNC CATGCCCTGN AGCCGGCTGC CGGCATCCTT GCCTGNTNC CTGCACTCGG	120
NCTGCTGTC TGGGGACCCG GNCAGCTATA GGCTCTGGGG GGNCCCGATG CAGCCCACAN	180
TGGGTGTGGT GCCCCAAGGC TTGTGGCANT NNTAANAGAN CTGGGNCCAG TGGGAGGCTT	240
NTCTNGGTAA A	251

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 288 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) IMMEDIATE SOURCE:

- (A) LIBRARY: BLADTUT02
- (B) CLONE: 1312529

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GTGACCATGA AGGCTGTGCT GCTTGCCCTG TTGATGGCAG GCTTGGCCCT GCAGCCAGGC	60
ACTGCCCTGC TGTGCTACTC CTGCAAAGCC CAGGTGAGCA ACGAGGACTG CCTGCAGGTG	120
GAGAACTGCA CCCAGCTGGG GGAGCAGTGC TGGACCGCGC GCATCCGCGC AGTTGGCCTC	180
CTGACCGTCA TCAGCAAAGG CTGCAGCTTG AACTGCGTGG ATGACTCACA GGACTACTAC	240
GTGGGCAAGA AGAACATCAC GTGCTGTGAC ACCGACTTGT GCAAGCCA	288

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 230 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) IMMEDIATE SOURCE:

- (A) LIBRARY: BLADTUT02
- (B) CLONE: 1314679

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GTGCTGTGAC ACCGACTTGT GCAACGCCAG CGGGGCCAT GCCCTGCAGC CGGCTGCCGC	60
CATCTTGCCTG CTGCTCCCTG CACTCGGCCT GCTGCTCTGG GGACCCGGCC AGCTATAAGGC	120
TCTGGGGGGC CCCGCTGCAG CCCACACTGG GTGTGGTGCC CCAGGCCTCT GTGCCACTCC	180
TCACAGACCT GGCCAGTGG GAGCCTGTCC TGGTCCCTGA GGCACATCCT	230

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 232 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

PF-0066 US

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BLADTUT02
- (B) CLONE: 1315052

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

TGACCATGAA GGCTGTGCTG CTTGCCCTGT TGATGGCAGG CTTGGCCCTG CAGCCAGGCA	60
CTGCCCTGCT GTGCTACTCC TGCAAAGCCC AGGTGAGCAA CGAGGACTGC CTGCAGGTGG	120
AGAACTGCAC CCAGCTGGGG GAGCAGTGCT GGACCGCGCG CATCCGCGCA GTTGGCCTCC	180
TGACCGTCAT CAACAAAAGG CTGCAGCTTG AACTGCGTGG ATGACTCACA GG	232

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BLADTUT02
- (B) CLONE: 1317088

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

CGGGGCCCAT GCCCTGCAGC CGGCTGCCGC CATCCTTGCG CTGCTCCCTG CACTCGGCCT	60
GCTGCTCTGG GGACCCG	77